

SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> A NOVEL CAROTENOID HYDROXYLASE GENE AND A METHOD FOR PRODUCING HYDROXY CAROTENOID AND A NOVEL GERANYLGERANYLPYROPHOSPHATE SYNTHETASE GENE

<130> FP-042PCT

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<151> 2003-11-26

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<151> 2004-06-03

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<170> PatentIn Ver. 2.1

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tcagaatgtc caccagcacg gcgtcgggcg accagtctc gacgatccgc aaccgctgt 11738

tgaccgttgc tgcggtcagg acttggcaac ccagccgttt cagcatctcc tccagatgaa 11798

gcagaaccag cgaatcgicc tcgatcacgc agactttcac gcccaacctc cagatgcat 11858
 cagggggaac taacggaiga atcccatgtt gcgtcaactc ggaagacggc gtttccgact 11918
 ggccatcgcc ttggcgggcg cggtcgtgac cctgcttctg gcggccactg gggtgacgct 11978
 gcaacgagaa ttc 11991

<210> 3
 <211> 774
 <212> DNA
 <213> Brevundimonas sp.

<220>
 <221> CDS
 <222> (1).. (771)

<400> 3
 atg ttg agg gat ctg ctc atc acc acc ctg gcg ctg agc ctg atc atc 48
 Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile
 1 5 10 15
 gcc ctg cgc tat ctg ctg gtc ggc gcg gcg gcc cat ggg ctg ctg tgg 96
 Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp
 20 25 30
 gcc ggg gcg ggc cgg gga cgg gcg ctg aac ctg cgg ccg ccg gcg atg 144
 Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met
 35 40 45
 aag cgc atc cgc gcc gag atc gtc gcc tcc ctg atc gcc tgc ccc atc 192
 Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile
 50 55 60
 tac gcc ctg ccg gcg gcc ctg gtg ctg gag ctg tgg aag cgg ggc ggg 240
 Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly
 65 70 75 80
 acg gcg atc tac agc gat ccc gac gcc tgg ccc ctg tgg tgg ctg ccg 288
 Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro
 85 90 95
 gtc agt ctg atc gtc tat ctg ctg gcg cac gac gcc ttc tac tac tgg 336
 Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp
 100 105 110

<210> 4
<211> 257
<212> PRT
<213> Brevundimonas sp.

<400> 4
Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile
1 5 10 15

Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp
 20 25 30

Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met
 35 40 45

Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile
 50 55 60

Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly
 65 70 75 80

Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro
 85 90 95

Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp
 100 105 110

Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala
 115 120 125

Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe
 130 135 140

Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala
 145 150 155 160

Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu
 165 170 175

Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro
 180 185 190

Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr
 195 200 205

His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr
 210 215 220

Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro
 225 230 235 240

Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu
 245 250 255

Arg

<210> 5
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 5
tacgaattcg atgcccctcg ccctg 25

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 6
tagaggatcc tcaaggagtg aactggatcg ta 32

<210> 7
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
tacgaattcg atgaccgccg ccgtcg 26

<210> 8
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8

tagaggatcc tcaagactcg ccgcccaca a 31

<210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 9
 tacgaattcg ctgtcgcgga tgcaggc 27

<210> 10
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 10
 tagaggatcc tgcggttcag cagccgataa aa 32

<210> 11
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 11
 tacgaattcg atgcgagcag cagtgatcgg a 31

<210> 12
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 12

tagaggatcc aagctcttgg agccctgct 29

<210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 13
 tacgaattcg atgagcgacg ccgtcct 27

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 14
 tagaggatcc tcagatgtgg gtccacagg 29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 15
 tacgaattcg atgatggcgg tggcgggc 28

<210> 16
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 16

tagaggatcc cccacatctg acggcgct 28

<210> 17
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 17
 tacgaattcg atgtccttca tctcttccgg c 31

<210> 18
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 18
 tagaggatcc accgccatca tgacgagg 28

<210> 19
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 19
 tacgaattcg atggcgatcg tcggcttaa 29

<210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 20

tagaggatcc ctagcgtcca agttcggcct 30

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 21
tacgaattcg atgcccaccc cgcacgacg 29

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 22
tagaggatcc tcagaagcgg ggctcttcca 30

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 23
tacgaattcg atggcctggc tgacgtggat 30

<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 24

tagaggatcc tcaggcgccg ctgctggaa 29

<210> 25
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 25
 tacgaattcg atgttgaggg atctgctcat ca 32

<210> 26
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 26
 tagaggatcc tcaccgaaga ggcgctgag 29

<210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 27
 tacgaattcg atgctgaaac ggctgggtt 29

<210> 28
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 28

tagaggatcc ctatttccag ttctgggacc g

31

<210> 29

<211> 486

<212> DNA

<213> Brevundimonas sp.

<220>

<221> CDS

<222> (1).. (483)

<400> 1

atg gcc tgg ctg acg tgg atc gcg ctg ttc ctg acc gcc ttt ttg ggc	48
Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly	
1 5 10 15	
atg gag gcg ttc gcc tgg atc atg cac cgc tat gtg atg cac ggt ttc	96
Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe	
20 25 30	
ctg tgg tcc tgg cac cgc agc cat cat gag ccg cac gat cac ccc ctg	144
Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu	
35 40 45	
gag aag aac gac ctg ttc gcc gtg gtc ttc gcc gcc ccg gcc atc gtc	192
Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val	
50 55 60	
atg gtg gcc gtg ggt ctg cac ctg tgg ccc tgg gcc ctg ccg gtc ggc	240
Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly	
65 70 75 80	
ctg ggg atc acg gcc tat ggg atg gtc tat ttc ttc ttc cac gac ggc	288
Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly	
85 90 95	
ctg gtg cac cgg cgg ttc ccg acg ggc ttt tcc ggg cgg tcc ggc ttc	336
Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe	
100 105 110	
tgg acg cgg cgc atc cag gcg cac cgt ctg cat cac gcc gtg cgc acg	384
Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr	
115 120 125	
cgc gaa ggc tgc gtc tcc ttc ggc ttt ctg tgg gtg cgg tcg gcg cgg	432
Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg	
130 135 140	

gcg ctg aag gcc gaa ctg gct cag aag cgg ggc tct tcc agc agc ggc 480
 Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly
 145 150 155 160

gcc tga 486
 Ala

<210> 30
 <211> 161
 <212> PRT
 <213> Brevundimonas sp.

<400> 30
 Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly
 1 5 10 15

Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe
 20 25 30

Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu
 35 40 45

Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val
 50 55 60

Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly
 65 70 75 80

Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly
 85 90 95

Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe
 100 105 110

Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr
 115 120 125

Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg
 130 135 140

Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly
 145 150 155 160

Ala

<210> 31
 <211> 897
 <212> DNA
 <213> Brevundimonas sp.

<220>
 <221> CDS
 <222> (1).. (894)

<400> 31
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 Met Ala Ile Val Gly Leu Arg Pro Gln Pro Val Ser Asp Pro Glu Pro
 1 5 10 15
 cag tcg ccc gag aat ctg cgt ggc ctg gtg cag gac cgg ctg gcc gag 96
 Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu
 20 25 30
 acg gcg ccc tca tcg gac ggt ctt tta gcc ctc gcc gcg cgc gag gcc 144
 Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala
 35 40 45
 ctg ctg gga ccg ggc aag cgg gtc agg ccg gtc gtg gcc atg ttg gcc 192
 Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala
 50 55 60
 gcc gcg cac gtc ggc ggg cgg gcc gag gac gcc ctg gat ttc ggt tgc 240
 Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys
 65 70 75 80
 gcg gtc gaa atg gcc cat gcc gcc tcc ctg gtt ctg gac gac ctg ccc 288
 Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro
 85 90 95
 tgt atg gat gat gcg gcc ttg cgg cgc ggt cag ccg acc ctg cac cgc 336
 Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg
 100 105 110
 cgc cac ggc gag gat gcg gcc gtg ctg gcg gcc gtg gcc ctt ttg aac 384
 Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn
 115 120 125
 caa tcg acc cgg ctg att ctg caa agc cgg gcg ccg tcg gag gcg cgg 432
 Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg
 130 135 140
 ctg ggc gcc ctg gac gat ttg acg cag gcg atc ggc ttc gac ggc ctg 480

Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu
 145 150 155 160
 gcc gag ggc cag atg cgc gat ctg cgc gac gat ccc gtt cag cgc gac 528
 Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp
 165 170 175
 gtg gtc gcc ctg cgt cgg atc aac gat ctg aag acc ggc gcc ctg ttc 576
 Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe
 180 185 190
 gtc gcg gcc gcg cgg ggc ggc ggc cgg atg ggc ggc ggc gat gcg gac 624
 Val Ala Ala Ala Arg Gly Gly Gly Arg Met Gly Gly Gly Asp Ala Asp
 195 200 205
 gac ctg gcg cgt ctc gcc gcc ttc ggc gaa gcg gtc ggc ttc gcc ttc 672
 Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe
 210 215 220
 cag ctt tgc gac gac ctg atg gac gcc tgt tgc acg agc gag gcc ttg 720
 Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu
 225 230 235 240
 ggc aag gac gtg ggt cag gat cag ggc gtg acc acc ttc gtg gac ctg 768
 Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu
 245 250 255
 tgg ggc gaa ggc cgg gtc cgc gcc ggg gtg cgc cag tca ctg gcc cgg 816
 Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg
 260 265 270
 gcg gcc gag gcg gtc ggg cac gac agc ccc ctg acg acc tat gtc ctt 864
 Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu
 275 280 285
 cat ctc ttc cgg cag gcc gaa ctt gga cgc tag 897
 His Leu Phe Arg Gln Ala Glu Leu Gly Arg
 290 295

<210> 32
 <211> 298
 <212> PRT
 <213> Brevundimonas sp.

<400> 32
 Met Ala Ile Val Gly Leu Arg Pro Gln Pro Val Ser Asp Pro Glu Pro
 1 5 10 15

Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu
 20 25 30
 Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala
 35 40 45
 Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala
 50 55 60
 Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys
 65 70 75 80
 Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro
 85 90 95
 Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg
 100 105 110
 Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn
 115 120 125
 Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg
 130 135 140
 Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu
 145 150 155 160
 Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp
 165 170 175
 Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe
 180 185 190
 Val Ala Ala Ala Arg Gly Gly Gly Arg Met Gly Gly Gly Asp Ala Asp
 195 200 205
 Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe
 210 215 220
 Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu
 225 230 235 240
 Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu
 245 250 255
 Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg
 260 265 270

Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu
275 280 285

His Leu Phe Arg Gln Ala Glu Leu Gly Arg
290 295